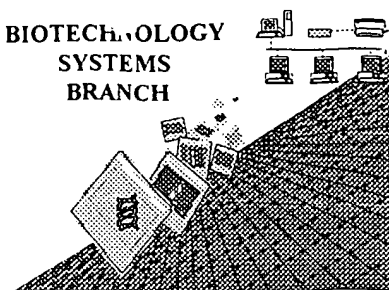


Fonda

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



#11
1/21?

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/435,770

Source: 1652

Date Processed by STIC: 1/24/2001

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FEB 02 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/435,770

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1652

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001

TIME: 14:32:13

Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

Does Not Comply
Corrected Diskette Needed

pg 1-15

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4 <110> APPLICANT: YAMAMOTO, Takuo
 5 MARUTA, Kazuhiko .
 6 KUBOTA, Michio
 7 FUKUDA, Shigeharu
 8 MIYAKE, Toshio
 10 <120> TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,
 11 TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING
 12 SACCHARIDES USING THE ENZYMES
 14 <130> FILE REFERENCE: YAMAMOTO=16A
 16 <140> CURRENT APPLICATION NUMBER: 09/435,770
 17 <141> CURRENT FILING DATE: 1999-11-08
 19 <150> PRIOR APPLICATION NUMBER: JP 258,394/1998
 20 <151> PRIOR FILING DATE: 1998-09-11
 22 <150> PRIOR APPLICATION NUMBER: JP 352,252/1998
 23 <151> PRIOR FILING DATE: 1998-12-11
 25 <150> PRIOR APPLICATION NUMBER: JP 16,931/1999
 26 <151> PRIOR FILING DATE: 1999-01-26
 28 <160> NUMBER OF SEQ ID NOS: 39
 30 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

241 <210> SEQ ID NO: 7
 242 <211> LENGTH: 2268
 243 <212> TYPE: DNA
 244 <213> ORGANISM: ARTHROBACTER sp.S34
 246 <400> SEQUENCE: 7

E--> 247 cccgccagta cctaccgcct tcagatctcg gcggagttca ccctcttcga cgcggcgcgc 60
 248 60
 E--> 249 atcgtgccct acctgcaccg cctcggcgcc gactggctgt acctctcgcc gctgctcgag 120
 250 120
 E--> 251 tccgagtcgg gtcctctgca cggctacgac gtggtcgacc actcccgcgt cgacgccgcc
 252 180
 E--> 253 cgcggcgggc cggaggggct cgccgagctc tcccgtgcgg cgcacgagcg cggcatgggc
 254 240
 E--> 255 gtcgtcgtcg acatcgtgcc caaccacgtc ggcgtcgca cgccgaaggc gaaccgctgg
 256 300
 E--> 257 tgggtgggacg ttctggcccc tggacagcgg tcggagtacg ccgactactt cgacatcgac
 258 360
 E--> 259 tgggagttcg gcggcggcag gctgcgcctg cccgtgctcg ggcagggccc cgacgagctc
 260 420
 E--> 261 gacgcgctga gagtggatgg cgacgagctc gtctactacg agcaccgctt cccgacgcgc
 262 480
 E--> 263 gagggcaccg gcggcggcac cccgcgcgag gtgcacgacc ggcagcacta cgagctgatg
 264 540
 E--> 265 tcgtggcggc gggccgacca cgacctcaac taccgccgct tcttcgccgt gaacacgctc

(see
 item 1 on
 Error summary
 sheet)

global
 format error

RAW SEQUENCE LISTING

DATE: 01/24/2001

PATENT APPLICATION: US/09/435,770

TIME: 14:32:13

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\01242001\I435770.raw

266 600
E--> 267 gccgccgtac gcgtcgaaga cccgcgcgtg ttcgacgaca cccaccgcga gatcggccgc
268 660
E--> 269 tggatcgccg agggcctcgt cgacggcctg cgcgtcgacc accccgcacgg gctgcgcgcc
270 720
E--> 271 cccggcgact acctgcgccg tctcgccgag ctgcaccaag gcaggccgat ctgggtcgag
272 780
E--> 273 aagatcatcg agggcgacga gcggatgccc ccgcagtggc ccatcgccgg caccaccggc
274 840
E--> 275 tacgacgcgc tggccgggat cgaccgggtg ctgctcgacc ccgcgggcga gcatccgctc
276 900
E--> 277 acccagatcg tcgacgaggc ggcaggcagc ccccggcgct gggccgagct ggttcccag
278 960
E--> 279 cgcaagcggg ccgtcgcccg cggcattctg aactccgaga tccgccgcgt cggccgcgaa
280 1020
E--> 281 ctcgagagag tcgccggcga cgtcgaagac gcgctcgctg agatcgccgc cgccctgtcc
282 1080
E--> 283 gtctaccgca gctacctgcc gtccgggcgc gagcacctcg acgaagccgt ggccgcgcgc
284 1140
E--> 285 caggccgcag ccccccagct cgaggccgac ctgcgcccg tcggcgcagc gctcgccgac
286 1200
E--> 287 ccgggcaacc ccgcgcgct ccgcttcag cagaccagcg gcatgatcat ggccaagggc
288 1260
E--> 289 gtcgaggaca acgcgttcta ccgctacccc cggctcacct cgctgaccga ggtcggggga
290 1320
E--> 291 gaccgcagcc tgttcgcgat cgacgcggcc gccttcacg cggcgcagcg cgaccgcgcc
292 1380
E--> 293 gcccggtgc ccgagtcgat gacgacgctg accaccacg acaccaagcg cagcgaagac
294 1440
E--> 295 acccgggcgc ggatcacgc gtcgcccag gccccgaac gctggcggcg ctctctgacc
296 1500
E--> 297 gaggtcggcg ggctcatcg aacgggcgac cgggtgctgg agaacctgat ctggcaggcg
298 1560
E--> 299 atcgtcggcg cgtggccggc gagccgggag cggctcgagg cctacgcgct gaaggccgcg
300 1620
E--> 301 cgcgaagccg gcgagtcgac cgactggatc gacggcgacc ccgcgttcga agagcggctg
302 1680
E--> 303 accgcctgg tcacggtcgc cgtcgaggag ccgctcgtgc acgagctgct cgagcggctc
304 1740
E--> 305 gtcgacgagc tgacggcggc cgggtactcc aacggcctcg cggcgaagct gctgcagctg
306 1800
E--> 307 ctgcccccg gaacccccga cgtgtaccag ggcacggaac gctgggaccg gtcgctggtg
308 1860
E--> 309 gaccgggaca accgtcgcgc cgtggatttc gccgcggcat ccgagctgct cgaccgcctc
310 1920
E--> 311 gacggcggtc ggcggccgcc cgtcgacgag accggcgcg tcaagacgct cgtcgtctcc
312 1980
E--> 313 cgcgcgctgc ggtcgcgcc cgaccggccc gagctgttca ccgcgtacca cccggtcacg
314 2040

*same
even*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001

TIME: 14:32:13

Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

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E--> 315 gcgcgcggcg cgcaggccga gcacctgatc ggcttcgacc gcggcgggcg gatcgccctg
 316 2100
 E--> 317 gccaccgcc tgcgcctcgg cctcgccgcc gcaggcggtt gggcgacac ggtcgtcgac
 318 2160
 E--> 319 gtcggcgagc ggagcctcgg cgacgagctg accggccgcg aggcccgcg agcggcgcgc
 320 2220
 E--> 321 gtggccgagt tgttcgccga ctaccccgtc gccttctggt tggagaca
 322 2268
 325 <210> SEQ ID NO: 8
 326 <211> LENGTH: 28
 327 <212> TYPE: DNA
 328 <213> ORGANISM: ARTHROBACTER sp.S34
 330 <400> SEQUENCE: 8
 E--> 331 tttttaata aaatcaggag gaaaaaat
 332 28
 529 <210> SEQ ID NO: 17
 530 <211> LENGTH: 1725
 531 <212> TYPE: DNA
 532 <213> ORGANISM: ARTHROBACTER sp.S34
 534 <400> SEQUENCE: 17
 E--> 535 atgaaccgac gattcccggt ctgggcgccc caggccgcgc aggtgacgct cgtcgtgggc
 536 60
 E--> 537 caaggccgcg ccgaactccc gctgaccgcg gacgagaacg gatgggtgggc tcttcagcag
 538 120
 E--> 539 ccgtgggacg gcggccccga cctcgtcgac tacggctacc tcgtcgacgg caagggtccc
 540 180
 E--> 541 ttcgccgacc cgcggtcgct gcggcagccg cgcggcgtgc acgagctcgg ccgcgaattc
 542 240
 E--> 543 gaccccgccc gctacgcgtg gggcgacgac ggatggcgcg gccgagacct caccggagcc
 544 300
 E--> 545 gtgatctacg aactgcacgt cggcaccttc acccctgagg gaacgctgga cagcgccatc
 546 360
 E--> 547 cgtcgctcgc accacctggt gcgcctcggc gtcgacgcgg tcgagctgct gcccgtcaac
 548 420
 E--> 549 gcgttcaacg gcacccacgg ctggggctac gacggggtgc tctggtacgc ggtgcacgag
 550 480
 E--> 551 ccctacggcg gcccgaggc gtaccagcgc ttcgtcgacg cctgccacgc ccgcggcctc
 552 540
 E--> 553 gcgctcgtgc aggacgtcgt ctacaaccac ctgggcccga gcggcaacca cctgcccgcg
 554 600
 E--> 555 ttcggccctt acctcgggtc gggcgccgcc aacacctggg gcgacgcgct gaacctcgac
 556 660
 E--> 557 gggccgctct ccgacgaggt gcggcggtac atcatcgaca acgcggtgta ctggtcgcg
 558 720
 E--> 559 gacatgcacg ccgacgggct gcggctcgac gccgtgcacg cgtcgcgcga cggccgcgcg
 560 780
 E--> 561 ctgcacctgc tcgaagagct cggcgccgcg gtcgacgagc tggcgggcga gtcgggcccg
 562 840
 E--> 563 ccgctgacgc tcctcgccga gagcgacctg aacgacccga agctgatccg ctcccgcgcg

same

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001

TIME: 14:32:13

Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

564 900
E--> 565 gcgcacggct acggcctcga cgcccagtgg gacgacgacg tgcaccacgc ggtgcacgcc
566 960
E--> 567 aacgtgaccg gcgagaccgt cggctactac gccgacttcg gcgggctcgg cgccctcgtc
568 1020
E--> 569 aaggtgttcc agcgcggctg gtccacgac ggcacctggt cgagcttcgg cgagcggcac
570 1080
E--> 571 cagggccggc cgctcgaccc cgacatcccc ttccgccggc tcgtcgctt cgcgcaggat
572 1140
E--> 573 cagcaccagg tcggcaaccg agcggtcggc gaccgcatgt cggcgcaggc cggcgagggt
574 1200
E--> 575 tcgtcgcggc ccgcggcggc gctcgtgctg ctccggcccgt tcaccccgat gctgttcacg
576 1260
E--> 577 ggcgaggagt ggggcgcgcg caccctgtgg cagttcttca cctcccaccc cgagcccgag
578 1320
E--> 579 ctgggggagg cgacggcgcg cgggcgcacg gccgagttcg cccgcatggg ctgggacccg
580 1380
E--> 581 gcagtcgtgc ccgacccgca ggaccggcc accttcgccc gctcgcacct ggactggtcc
582 1440
E--> 583 gagcccgagc ggggaaccgca cgcgggcctg ctgccttct acaccgacct gatcgcgctg
584 1500
E--> 585 cggcgcgagc tgccggtcga tgcgccggcg cgcgagggtg atgccgacga ggcgcgcggc
586 1560
E--> 587 gtcttcgcgt tcagccgcgg cccgctgcgg gtcacggtcg cgctgcgccc cggaccggtc
588 1620
E--> 589 ggggtgcccc agcacggggg cctcgtgctc gcctacggcg aggtgcgcgc cggcgcggcc
590 1680
E--> 591 ggactgcacc tcgacggggc gggagccgcg atcgtgcgcc tcgag
592 1725
595 <210> SEQ ID NO: 18
596 <211> LENGTH: 23
597 <212> TYPE: DNA
598 <213> ORGANISM: ARTHROBACTER sp.S34
600 <400> SEQUENCE: 18
E--> 601 gcsaaccgst ggtggtggga cgt
602 23
605 <210> SEQ ID NO: 19
606 <211> LENGTH: 3252
607 <212> TYPE: DNA
608 <213> ORGANISM: ARTHROBACTER sp.S34
610 <220> FEATURE:
611 <221> NAME/KEY: 5'UTR
612 <222> LOCATION: (1)..(742)
614 <220> FEATURE:
615 <221> NAME/KEY: CDS
616 <222> LOCATION: (743)..(3013)
618 <220> FEATURE:
619 <221> NAME/KEY: 3'UTR
620 <222> LOCATION: (742)..(3014)

RAW SEQUENCE LISTING

DATE: 01/24/2001

PATENT APPLICATION: US/09/435,770

TIME: 14:32:13

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\01242001\I435770.raw

622 <400> SEQUENCE: 19

E--> 623 atgccgacga cgaacttgag cgcgttctcg ggcacccgcg agagcgggcc gcgcacggcg
 624 60
 E--> 626 gcgcccagtg ccacgacgag cagcatcgcg gcgagcgccg cgacgacggc gaccggcagg
 627 120
 E--> 629 cgcccctgat tgctggcgaa ggtgagcacg atgaagacca cctcgaggcc ctcgagcaac
 630 180
 E--> 632 acacctttga acgacacggt gaacgcgtac caatcgga ccccgaaaccg gctctcgcg
 633 240
 E--> 635 cgggcgctct cggccgcctc gacctgacgc cggaaggcag cctcctcgtc acggagagcc
 636 300
 E--> 638 ctgcgccctg ccgcgcgcag caccgccttg cgcagccagc cgagcccga gacgagcagc
 639 360
 E--> 641 aaccggccga cgacgaggcg cagcacggcc agcggcagca gcaggatcg gggaccgacg
 642 420
 E--> 644 agcgcgacgg ccgcggccag caccaccacg gcgacggcgg cacctgtcag cggcgaccgc
 645 480
 E--> 647 cagctgcggg tggcgccgac cgcgacgacg atcgtggtcg cctccaccgc ctcgaccacg
 648 540
 E--> 650 caggcgagga acacggcggc gaacagggcg acggcgggtca tcggcccagc agacggttga
 651 600
 E--> 653 ccatacacggc acgctagcgc cattgtcac aggaagggcc aagacgcccg caacgcggca
 654 660
 E--> 656 cccgtggacg gcgcgtaccg gcgtgtgacc gatcgtgtca accggtggcg cccgccccga
 657 720
 E--> 659 gcacctgcgt agattcggcc tc gtg ccc gcc agt acc tac cgc ctt cag atc
 660 772
 661 Met Pro Ala Ser Thr Tyr Arg Leu Gln Ile
 662 1 5 10
 E--> 664 tcg gcg gag ttc acc ctc ttc gac gcg gcg cgc atc gtg ccc tac ctg
 665 820
 666 Ser Ala Glu Phe Thr Leu Phe Asp Ala Ala Arg Ile Val Pro Tyr Leu
 667 15 20 25
 E--> 669 cac cgc ctc ggc gcc gac tgg ctg tac ctc tcg ccg ctg ctc gag tcc
 670 868
 671 His Arg Leu Gly Ala Asp Trp Leu Tyr Leu Ser Pro Leu Leu Glu Ser
 672 30 35 40
 E--> 674 gag tcg ggc tcc tcg cac ggc tac gac gtg gtc gac cac tcc cgc gtc
 675 916
 676 Glu Ser Gly Ser Ser His Gly Tyr Asp Val Val Asp His Ser Arg Val
 677 45 50 55
 E--> 679 gac gcc gcc cgc ggc ggg ccg gag ggg ctc gcc gag ctc tcc cgt gcg
 680 964
 681 Asp Ala Ala Arg Gly Gly Pro Glu Gly Leu Ala Glu Leu Ser Arg Ala
 682 60 65 70
 E--> 684 gcg cac gag cgc ggc atg ggc gtc gtc gtc gac atc gtg ccc aac cac
 685 1012
 686 Ala His Glu Arg Gly Met Gly Val Val Val Asp Ile Val Pro Asn His
 687 75 80 85 90

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001

TIME: 14:32:13

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\01242001\I435770.raw

```

E--> 689 gtc ggc gtc gcg acg ccg aag gcg aac cgc tgg tgg tgg gac gtt ctg
      690 1060
      691 Val Gly Val Ala Thr Pro Lys Ala Asn Arg Trp Trp Trp Asp Val Leu
      692                      95                      100                      105
E--> 694 gcc cgt gga cag cgg tcg gag tac gcc gac tac ttc gac atc gac tgg
      695 1108
      696 Ala Arg Gly Gln Arg Ser Glu Tyr Ala Asp Tyr Phe Asp Ile Asp Trp
      697                      110                      115                      120
E--> 699 gag ttc ggc ggc ggc agg ctg cgc ctg ccc gtg ctc ggc gac ggc ccc
      700 1156
      701 Glu Phe Gly Gly Gly Arg Leu Arg Leu Pro Val Leu Gly Asp Gly Pro
      702                      125                      130                      135
E--> 704 gac gag ctc gac gcg ctg aga gtg gat ggc gac gag ctc gtc tac tac
      705 1204
      706 Asp Glu Leu Asp Ala Leu Arg Val Asp Gly Asp Glu Leu Val Tyr Tyr
      707          140                      145                      150
E--> 709 gag cac cgc ttc ccg atc gcc gag ggc acc ggc ggc ggc acc ccg cgc
      710 1252
      711 Glu His Arg Phe Pro Ile Ala Glu Gly Thr Gly Gly Gly Thr Pro Arg
      712 155                      160                      165                      170
E--> 714 gag gtg cac gac cgg cag cac tac gag ctg atg tcg tgg cgg cgg gcc
      715 1300
      716 Glu Val His Asp Arg Gln His Tyr Glu Leu Met Ser Trp Arg Arg Ala
      717                      175                      180                      185
E--> 719 gac cac gac ctc aac tac cgc cgc ttc ttc gcc gtg aac acg ctc gcc
      720 1348
      721 Asp His Asp Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala
      722                      190                      195                      200
E--> 724 gcc gta cgc gtc gaa gac ccg cgc gtg ttc gac gac acc cac cgc gag
      725 1396
      726 Ala Val Arg Val Glu Asp Pro Arg Val Phe Asp Asp Thr His Arg Glu
      727          205                      210                      215
E--> 729 atc ggc cgc tgg atc gcc gag ggc ctc gtc gac ggc ctg cgc gtc gac
      730 1444
      731 Ile Gly Arg Trp Ile Ala Glu Gly Leu Val Asp Gly Leu Arg Val Asp
      732          220                      225                      230
E--> 734 cac ccc gac ggg ctg cgc gcc ccc ggc gac tac ctg cgc cgt ctc gcc
      735 1492
      736 His Pro Asp Gly Leu Arg Ala Pro Gly Asp Tyr Leu Arg Arg Leu Ala
      737 235                      240                      245                      250
E--> 739 gag ctc gcc caa ggc agg ccg atc tgg gtc gag aag atc atc gag ggc
      740 1540
      741 Glu Leu Ala Gln Gly Arg Pro Ile Trp Val Glu Lys Ile Ile Glu Gly
      742          255                      260                      265
E--> 744 gac gag cgg atg ccc ccg cag tgg ccc atc gcc ggc acc acc ggc tac
      745 1588
      746 Asp Glu Arg Met Pro Pro Gln Trp Pro Ile Ala Gly Thr Thr Gly Tyr
      747          270                      275                      280
E--> 749 gac gcg ctg gcc ggg atc gac cgg gtg ctc gtc gac ccc gcg ggc gag

```


RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770

DATE: 01/24/2001

TIME: 14:32:13

Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\01242001\I435770.raw

```

750 1636
751 Asp Ala Leu Ala Gly Ile Asp Arg Val Leu Val Asp Pro Ala Gly Glu
752          285          290          295
E--> 754 cat ccg ctc acc cag atc gtc gac gag gcg gca ggc agc ccc cgg cgc
755 1684
756 His Pro Leu Thr Gln Ile Val Asp Glu Ala Ala Gly Ser Pro Arg Arg
757      300          305          310
E--> 759 tgg gcc gag ctg gtt ccc gag cgc aag cgg gcc gtc gcc cgc ggc atc
760 1732
761 Trp Ala Glu Leu Val Pro Glu Arg Lys Arg Ala Val Ala Arg Gly Ile
762 315          320          325          330
E--> 764 ctg aac tcc gag atc cgc cgc gtc gcc cgc gaa ctc gga gag gtc gcc
765 1780
766 Leu Asn Ser Glu Ile Arg Arg Val Ala Arg Glu Leu Gly Glu Val Ala
767          335          340          345
E--> 769 ggc gac gtc gaa gac gcg ctc gtc gag atc gcc gcc gcc ctg tcc gtc
770 1828
771 Gly Asp Val Glu Asp Ala Leu Val Glu Ile Ala Ala Ala Leu Ser Val
772          350          355          360
E--> 774 tac cgc agc tac ctg ccg ttc ggg cgc gag cac ctc gac gaa gcc gtg
775 1876
776 Tyr Arg Ser Tyr Leu Pro Phe Gly Arg Glu His Leu Asp Glu Ala Val
777          365          370          375
E--> 779 gcc gcc gcg cag gcc gca gcc ccc cag ctc gag gcc gac ctc gcc gcc
780 1924
781 Ala Ala Ala Gln Ala Ala Ala Pro Gln Leu Glu Ala Asp Leu Ala Ala
782      380          385          390
E--> 784 gtc ggc gca gcg ctc gcc gac ccg ggc aac ccc gcc gcg ctc cgc ttc
785 1972
786 Val Gly Ala Ala Leu Ala Asp Pro Gly Asn Pro Ala Ala Leu Arg Phe
787 395          400          405          410
E--> 789 cag cag acc agc ggc atg atc atg gcc aag ggc gtc gag gac aac gcg
790 2020
791 Gln Gln Thr Ser Gly Met Ile Met Ala Lys Gly Val Glu Asp Asn Ala
792          415          420          425
E--> 794 ttc tac cgc tac ccc cgg ctc acc tcg ctg acc gag gtc ggg gga gac
795 2068
796 Phe Tyr Arg Tyr Pro Arg Leu Thr Ser Leu Thr Glu Val Gly Gly Asp
797          430          435          440
E--> 799 ccg agc ctg ttc gcg atc gac gcg gcc gcc ttc cac gcg gcg cag cgc
800 2116
801 Pro Ser Leu Phe Ala Ile Asp Ala Ala Ala Phe His Ala Ala Gln Arg
802          445          450          455
E--> 804 gac cgc gcc gcc cgg ctg ccc gag tcg atg acg acg ctg acc acc cac
805 2164
806 Asp Arg Ala Ala Arg Leu Pro Glu Ser Met Thr Thr Leu Thr Thr His
807      460          465          470
E--> 809 gac acc aag cgc agc gaa gac acc cgg gcg cgg atc acc gcg ctc gcc
810 2212

```

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Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\01242001\I435770.raw

```

      811 Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Thr Ala Leu Ala
      812 475                               480                               485                               490
E--> 814 gag gcc ccc gaa cgc tgg cgg cgc ttc ctg acc gag gtc ggc ggg ctc
      815 2260
      816 Glu Ala Pro Glu Arg Trp Arg Arg Phe Leu Thr Glu Val Gly Gly Leu
      817                               495                               500                               505
E--> 819 atc gga acg ggc gac cgg gtg ctg gag aac ctg atc tgg cag gcg atc
      820 2308
      821 Ile Gly Thr Gly Asp Arg Val Leu Glu Asn Leu Ile Trp Gln Ala Ile
      822                               510                               515                               520
E--> 824 gtc ggc gcg tgg ccg gcg agc cgg gag cgg ctc gag gcc tac gcg ctg
      825 2356
      826 Val Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Glu Ala Tyr Ala Leu
      827                               525                               530                               535
E--> 829 aag gcc gcg cgc gaa gcc ggc gag tcg acc gac tgg atc gac ggc gac
      830 2404
      831 Lys Ala Ala Arg Glu Ala Gly Glu Ser Thr Asp Trp Ile Asp Gly Asp
      832                               540                               545                               550
E--> 834 ccc gcg ttc gaa gag cgg ctg acc cgc ctg gtc acg gtc gcc gtc gag
      835 2452
      836 Pro Ala Phe Glu Glu Arg Leu Thr Arg Leu Val Thr Val Ala Val Glu
      837 555                               560                               565                               570
E--> 839 gag ccg ctc gtg cac gag ctg ctc gag cgg ctc gtc gac gag ctg acg
      840 2500
      841 Glu Pro Leu Val His Glu Leu Leu Glu Arg Leu Val Asp Glu Leu Thr
      842                               575                               580                               585
E--> 844 gcg gcc ggg tac tcc aac ggc ctc gcg gcg aag ctg ctg cag ctg ctc
      845 2548
      846 Ala Ala Gly Tyr Ser Asn Gly Leu Ala Ala Lys Leu Leu Gln Leu Leu
      847                               590                               595                               600
E--> 849 gcc ccc gga acc ccc gac gtg tac cag ggc acg gaa cgc tgg gac cgg
      850 2596
      851 Ala Pro Gly Thr Pro Asp Val Tyr Gln Gly Thr Glu Arg Trp Asp Arg
      852                               605                               610                               615
E--> 854 tcg ctg gtg gac ccg gac aac cgt cgc ccc gtg gat ttc gcc gcg gca
      855 2644
      856 Ser Leu Val Asp Pro Asp Asn Arg Arg Pro Val Asp Phe Ala Ala Ala
      857 620                               625                               630
E--> 859 tcc gag ctg ctc gac cgc ctc gac ggc ggc tgg cgg ccg ccc gtc gac
      860 2692
      861 Ser Glu Leu Leu Asp Arg Leu Asp Gly Gly Trp Arg Pro Pro Val Asp
      862 635                               640                               645                               650
E--> 864 gag acc ggc gcg gtc aag acg ctc gtc gtc tcc cgc gcg ctg cgg ctg
      865 2740
      866 Glu Thr Gly Ala Val Lys Thr Leu Val Val Ser Arg Ala Leu Arg Leu
      867                               655                               660                               665
E--> 869 cgc cgc gac cgg ccc gag ctg ttc acc gcg tac cac ccg gtc acg gcg
      870 2788
      871 Arg Arg Asp Arg Pro Glu Leu Phe Thr Ala Tyr His Pro Val Thr Ala

```

RAW SEQUENCE LISTING

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Input Set : A:\Yamamtol.app

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```

      872          670          675          680
E--> 874 cgc ggc gcg cag gcc gag cac ctg atc ggc ttc gac cgc ggc ggc gcg
      875 2836
      876 Arg Gly Ala Gln Ala Glu His Leu Ile Gly Phe Asp Arg Gly Gly Ala
      877          685          690          695
E--> 879 atc gcc ctg gcc acc cgc ctg ccg ctc ggc ctc gcc gcc gca ggc ggc
      880 2884
      881 Ile Ala Leu Ala Thr Arg Leu Pro Leu Gly Leu Ala Ala Ala Gly Gly
      882          700          705          710
E--> 884 tgg ggc gac acg gtc gtc gac gtc ggc gag cgg agc ctg cgc gac gag
      885 2932
      886 Trp Gly Asp Thr Val Val Asp Val Gly Glu Arg Ser Leu Arg Asp Glu
      887 715          720          725          730
E--> 889 ctg acc ggc cgc gag gcc cgc gga gcg gcg cgc gtg gcc gag ttg ttc
      890 2980
      891 Leu Thr Gly Arg Glu Ala Arg Gly Ala Ala Arg Val Ala Glu Leu Phe
      892          735          740          745
E--> 894 gcc gac tac ccc gtc gcc ctg ctg gtg gag aca tgaaccgacg attccccggtc
      895 3033
      896 Ala Asp Tyr Pro Val Ala Leu Leu Val Glu Thr
      897          750          755
E--> 899 tgggcgcccc aggcgcgcga ggtgacgctc gtcgtgggcc aaggccgcgc cgaactccccg
      900 3093
E--> 902 ctgaccgcgc acgagaacgg atggtgggct cttcagcagc cgtgggacgg cgccccgcgac
      903 3153
E--> 905 ctcgtcgact acggctacct cgtcgacggc aaggggcccct tcgccgaccc gcggtcgctg
      906 3213
E--> 908 cggcagccgc gcggcgtgca cgagctcggc cgcgaattc
      909 3252
      913 <210> SEQ ID NO: 20
      914 <211> LENGTH: 26
      915 <212> TYPE: DNA
      916 <213> ORGANISM: Artificial Sequence
      918 <220> FEATURE:
      919 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
      921 <400> SEQUENCE: 20
E--> 922 atgcccgcga gtacctaccg ccttca
      923 26
      926 <210> SEQ ID NO: 21
      927 <211> LENGTH: 25
      928 <212> TYPE: DNA
      929 <213> ORGANISM: Artificial Sequence
      931 <220> FEATURE:
      932 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
      934 <400> SEQUENCE: 21
E--> 935 tcatgtctcc accagcaggg cgacg
      936 25
      939 <210> SEQ ID NO: 22
      940 <211> LENGTH: 50

```

RAW SEQUENCE LISTING

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Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

941 <212> TYPE: DNA
942 <213> ORGANISM: Artificial Sequence
944 <220> FEATURE:
945 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
947 <400> SEQUENCE: 22
E--> 948 aattcttttt taataaaatc aggaggaatc tagatgttta ctagtctgca
949 50
952 <210> SEQ ID NO: 23
953 <211> LENGTH: 42
954 <212> TYPE: DNA
955 <213> ORGANISM: Artificial Sequence
957 <220> FEATURE:
958 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
960 <400> SEQUENCE: 23
E--> 961 gactagtaaa catctagatt cctcctgatt ttattaaaaa ag
962 42
965 <210> SEQ ID NO: 24
966 <211> LENGTH: 33
967 <212> TYPE: DNA
968 <213> ORGANISM: Artificial Sequence
970 <220> FEATURE:
971 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
973 <400> SEQUENCE: 24
E--> 974 aaatctagat gcccgccagt acctaccgcc ttc
975 33
978 <210> SEQ ID NO: 25
979 <211> LENGTH: 33
980 <212> TYPE: DNA
981 <213> ORGANISM: Artificial Sequence
983 <220> FEATURE:
984 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
986 <400> SEQUENCE: 25
E--> 987 aaaactagtt tatcatgtct ccaccagcag ggc
988 33
991 <210> SEQ ID NO: 26
992 <211> LENGTH: 22
993 <212> TYPE: DNA
994 <213> ORGANISM: Artificial Sequence
996 <220> FEATURE:
997 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
999 <400> SEQUENCE: 26
E--> 1000 atcgggtgatg tcggcgatat ag
1001 22
1004 <210> SEQ ID NO: 27
1005 <211> LENGTH: 29
1006 <212> TYPE: DNA
1007 <213> ORGANISM: Artificial Sequence
1009 <220> FEATURE:
1010 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC



RAW SEQUENCE LISTING

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Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

1012 <400> SEQUENCE: 27
E--> 1013 gtactggcgg gcatattttt tcctcctga
1014 29
1017 <210> SEQ ID NO: 28
1018 <211> LENGTH: 31
1019 <212> TYPE: DNA
1020 <213> ORGANISM: Artificial Sequence
1022 <220> FEATURE:
1023 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1025 <400> SEQUENCE: 28
E--> 1026 aatcaggagg aaaaaatatg cccgccagta c
1027 31
1030 <210> SEQ ID NO: 29
1031 <211> LENGTH: 22
1032 <212> TYPE: DNA
1033 <213> ORGANISM: Artificial Sequence
1035 <220> FEATURE:
1036 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1038 <400> SEQUENCE: 29
E--> 1039 tcgacgatct gggtgagcgg at
1040 22
1043 <210> SEQ ID NO: 30
1044 <211> LENGTH: 22
1045 <212> TYPE: DNA
1046 <213> ORGANISM: Artificial Sequence
1048 <220> FEATURE:
1049 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1051 <400> SEQUENCE: 30
E--> 1052 tcgacgagca cccggtcgat cc
1053 22
1056 <210> SEQ ID NO: 31
1057 <211> LENGTH: 26
1058 <212> TYPE: DNA
1059 <213> ORGANISM: Artificial Sequence
1061 <220> FEATURE:
1062 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1064 <400> SEQUENCE: 31
E--> 1065 cartgggag aygagtgatca ycaygc
1066 26
1069 <210> SEQ ID NO: 32
1070 <211> LENGTH: 2218
1071 <212> TYPE: DNA
1072 <213> ORGANISM: Artificial Sequence
1074 <220> FEATURE:
1075 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1077 <220> FEATURE:
1078 <221> NAME/KEY: CDS
1079 <222> LOCATION: (477)..(2201)
1081 <220> FEATURE:

same

see item 10 on Ena Summary sheet

RAW SEQUENCE LISTING

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Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

1082 <221> NAME/KEY: 3'UTR
 1083 <222> LOCATION: (2202)..(2218)
 E--> 1085 <400> SEQUENCE: 33
 E--> 1086 ctgcagctgc tcgcccccg aacccccgac gtgtaccagg gcacggaacg ctgggaccgg
 1087 60
 E--> 1089 tcgctggttg acccggaaca cgtcgcccc gtggatttcg ccgcggcacg cgagctgtct
 1090 120
 E--> 1092 gaccgcctcg acggcggtcg gcggcgcccc gtcgacgaga ccggcgcggt caagacgtct
 1093 180
 E--> 1095 gtcgtctccc gcgcgctgcg gctgcgcccc gaccggcccc agctgttcac cgcgtaccac
 1096 240
 E--> 1098 ccggtcacgg cgcgcggcgc gcaggccgag cacctgatcg gcttcgaccg cggcggcgcg
 1099 300
 E--> 1101 atcgccctgg ccaccgcct gccgctcggc ctgcgcgccg caggcggtcg gggcgacacg
 1102 360
 E--> 1104 gtcgtcgacg tcggcgagcg gagcctgcgc gacgagctga ccggccgcga ggcccgcgga
 1105 420
 E--> 1107 gcggcgcgcg tggccgagtt gttcgccgac taccctgctg ccctgctggt ggagac atg
 1108 479
 1109 Met
 1110 1
 E--> 1112 aac cga cga ttc ccg gtc tgg gcg ccc cag gcc gcg cag gtg acg ctc
 1113 527
 1114 Asn Arg Arg Phe Pro Val Trp Ala Pro Gln Ala Ala Gln Val Thr Leu
 1115 5 10 15
 E--> 1117 gtc gtg ggc caa ggc cgc gcc gaa ctc ccg ctg acc cgc gac gag aac
 1118 575
 1119 Val Val Gly Gln Gly Arg Ala Glu Leu Pro Leu Thr Arg Asp Glu Asn
 1120 20 25 30
 E--> 1122 gga tgg tgg gct ctt cag cag ccg tgg gac ggc ggc ccc gac ctc gtc
 1123 623
 1124 Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu Val
 1125 35 40 45
 E--> 1127 gac tac ggc tac ctc gtc gac ggc aag ggc ccc ttc gcc gac ccg cgg
 1128 671
 1129 Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro Arg
 1130 50 55 60 65
 E--> 1132 tcg ctg cgg cag ccg cgc ggc gtg cac gag ctc ggc cgc gaa ttc gac
 1133 719
 1134 Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe Asp
 1135 70 75 80
 E--> 1137 ccc gcc cgc tac gcg tgg ggc gac gac gga tgg cgc ggc cga gac ctc
 1138 767
 1139 Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp Leu
 1140 85 90 95
 E--> 1142 acc gga gcc gtg atc tac gaa ctg cac gtc ggc acc ttc acc cct gag
 1143 815
 1144 Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro Glu
 1145 100 105 110

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Input Set : A:\Yamamtol.app

Output Set: N:\CRF3\01242001\I435770.raw

E--> 1147 gga acg ctg gac agc gcc atc cgt cgc ctc gac cac ctg gtg cgc ctc
 1148 863
 1149 Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg Leu
 1150 115 120 125
 E--> 1152 ggc gtc gac gcg gtc gag ctg ctg ccc gtc aac gcg ttc aac ggc acc
 1153 911
 1154 Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly Thr
 1155 130 135 140 145
 E--> 1157 cac ggc tgg ggc tac gac ggg gtg ctc tgg tac gcg gtg cac gag ccc
 1158 959
 1159 His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu Pro
 1160 150 155 160
 E--> 1162 tac ggc ggc ccg gag gcg tac cag cgc ttc gtc gac gcc tgc cac gcc
 1163 1007
 1164 Tyr Gly Gly Pro Glu Ala Tyr Gln Arg Phe Val Asp Ala Cys His Ala
 1165 165 170 175
 E--> 1167 cgc ggc ctc gcc gtc gtg cag gac gtc gtc tac aac cac ctg ggc ccg
 1168 1055
 1169 Arg Gly Leu Ala Val Val Gln Asp Val Val Tyr Asn His Leu Gly Pro
 1170 180 185 190
 E--> 1172 agc ggc aac cac ctg ccc gac ttc ggc ccc tac ctc ggg tgc ggc gcc
 1173 1103
 1174 Ser Gly Asn His Leu Pro Asp Phe Gly Pro Tyr Leu Gly Ser Gly Ala
 1175 195 200 205
 E--> 1177 gcc aac acc tgg ggc gac gcg ctg aac ctc gac ggg ccg ctc tcc gac
 1178 1151
 1179 Ala Asn Thr Trp Gly Asp Ala Leu Asn Leu Asp Gly Pro Leu Ser Asp
 1180 210 215 220 225
 E--> 1182 gag gtg cgg cgg tac atc atc gac aac gcg gtg tac tgg ctg cgc gac
 1183 1199
 1184 Glu Val Arg Arg Tyr Ile Ile Asp Asn Ala Val Tyr Trp Leu Arg Asp
 1185 230 235 240
 E--> 1187 atg cac gcc gac ggg ctg cgg ctc gac gcc gtg cac gcg ctg cgc gac
 1188 1247
 1189 Met His Ala Asp Gly Leu Arg Leu Asp Ala Val His Ala Leu Arg Asp
 1190 245 250 255
 E--> 1192 gcc cgc gcg ctg cac ctg ctc gaa gag ctc gcc gcc cgc gtc gac gag
 1193 1295
 1194 Ala Arg Ala Leu His Leu Leu Glu Glu Leu Ala Ala Arg Val Asp Glu
 1195 260 265 270
 E--> 1197 ctg gcg ggc gag ctc ggc cgg ccg ctg acg ctc atc gcc gag agc gac
 1198 1343
 1199 Leu Ala Gly Glu Leu Gly Arg Pro Leu Thr Leu Ile Ala Glu Ser Asp
 1200 275 280 285
 E--> 1202 ctg aac gac ccg aag ctg atc cgc tcc cgc gcg gcg cac ggc tac ggc
 1203 1391
 1204 Leu Asn Asp Pro Lys Leu Ile Arg Ser Arg Ala Ala His Gly Tyr Gly
 1205 290 295 300 305
 E--> 1207 ctc gac gcc cag tgg gac gac gac gtg cac cac gcg gtg cac gcc aac

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Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

```

1208 1439
1209 Leu Asp Ala Gln Trp Asp Asp Asp Val His His Ala Val His Ala Asn
1210                               310                               315                               320
E--> 1212 gtg acc ggc gag acc gtc ggc tac tac gcc gac ttc ggc ggg ctc ggc
1213 1487
1214 Val Thr Gly Glu Thr Val Gly Tyr Tyr Ala Asp Phe Gly Gly Leu Gly
1215                               325                               330                               335
E--> 1217 gcc ctc gtc aag gtg ttc cag cgc ggc tgg ttc cac gac ggc acc tgg
1218 1535
1219 Ala Leu Val Lys Val Phe Gln Arg Gly Trp Phe His Asp Gly Thr Trp
1220                               340                               345                               350
E--> 1222 tcg agc ttc cgc gag cgg cac cac ggc cgg ccg ctc gac ccc gac atc
1223 1583
1224 Ser Ser Phe Arg Glu Arg His His Gly Arg Pro Leu Asp Pro Asp Ile
1225                               355                               360                               365
E--> 1227 ccg ttc cgc cgg ctc gtc gcc ttc gcg cag gat cac gac cag gtc ggc
1228 1631
1229 Pro Phe Arg Arg Leu Val Ala Phe Ala Gln Asp His Asp Gln Val Gly
1230                               370                               375                               380                               385
E--> 1232 aac cga gcg gtc ggc gac cgc atg tcg gcg cag gtc ggc gag ggt tcg
1233 1679
1234 Asn Arg Ala Val Gly Asp Arg Met Ser Ala Gln Val Gly Glu Gly Ser
1235                               390                               395                               400
E--> 1237 ctc gcc gcc gcg gcg gcg ctc gtg ctg ctc ggc ccg ttc acc ccg atg
1238 1727
1239 Leu Ala Ala Ala Ala Ala Leu Val Leu Leu Gly Pro Phe Thr Pro Met
1240                               405                               410                               415
E--> 1242 ctg ttc atg ggc gag gag tgg ggc gcg cgc acc ccg tgg cag ttc ttc
1243 1775
1244 Leu Phe Met Gly Glu Glu Trp Gly Ala Arg Thr Pro Trp Gln Phe Phe
1245                               420                               425                               430
E--> 1247 acc tcc cac ccc gag ccc gag ctg ggg gag gcg acg gcg cgc ggg cgc
1248 1823
1249 Thr Ser His Pro Glu Pro Glu Leu Gly Glu Ala Thr Ala Arg Gly Arg
1250                               435                               440                               445
E--> 1252 atc gcc gag ttc gcc cgc atg ggc tgg gac ccg gca gtc gtg ccc gac
1253 1871
1254 Ile Ala Glu Phe Ala Arg Met Gly Trp Asp Pro Ala Val Val Pro Asp
1255                               450                               455                               460                               465
E--> 1257 ccg cag gac ccg gcc acc ttc gcc cgc tcg cac ctg gac tgg tcc gag
1258 1919
1259 Pro Gln Asp Pro Ala Thr Phe Ala Arg Ser His Leu Asp Trp Ser Glu
1260                               470                               475                               480
E--> 1262 ccc gag cgg gaa ccg cac gcg ggc ctg ctc gcc ttc tac acc gac ctg
1263 1967
1264 Pro Glu Arg Glu Pro His Ala Gly Leu Leu Ala Phe Tyr Thr Asp Leu
1265                               485                               490                               495
E--> 1267 atc gcg ctg cgg cgc gag ctg ccg gtc gat gcg ccg gcg cgc gag gtg
1268 2015

```


RAW SEQUENCE LISTING

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Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

```

1269 Ile Ala Leu Arg Arg Glu Leu Pro Val Asp Ala Pro Ala Arg Glu Val
1270      500      505      510
E--> 1272 gat gcc gac gag gcg cgc ggc gtc ttc gcg ttc agc cgc ggc ccg ctg
1273 2063
1274 Asp Ala Asp Glu Ala Arg Gly Val Phe Ala Phe Ser Arg Gly Pro Leu
1275      515      520      525
E--> 1277 cgg gtc acg gtc gcg ctg cgc ccc gga ccg gtc ggg gtg ccc gag cac
1278 2111
1279 Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu His
1280 530      535      540      545
E--> 1282 ggg ggc ctc gtg ctc gcc tac ggc gag gtg cgc gcc ggc gcc gcc gga
1283 2159
1284 Gly Gly Leu Val Leu Ala Tyr Gly Glu Val Arg Ala Gly Ala Ala Gly
1285      550      555      560
E--> 1287 ctg cac ctc gac ggg ccg gga gcc gcg atc gtg cgc ctc gag
1288 2201
1289 Leu His Leu Asp Gly Pro Gly Ala Ala Ile Val Arg Leu Glu
1290      565      570      575
E--> 1292 tgacgcggct ggggtacc
1293 2218
1296 <210> SEQ ID NO: 33
1297 <211> LENGTH: 25
1298 <212> TYPE: DNA
1299 <213> ORGANISM: Artificial Sequence
1301 <220> FEATURE:
1302 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1304 <400> SEQUENCE: 33
E--> 1305 atgaaccgac gattcccggt ctggg
1306 25
1308 <210> SEQ ID NO: 34
1309 <211> LENGTH: 25
1310 <212> TYPE: DNA
1311 <213> ORGANISM: Artificial Sequence
1313 <220> FEATURE:
1314 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1316 <400> SEQUENCE: 34
E--> 1317 tcactcgagg cgcacgatcg cggt
1318 25

```



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/435,770

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Input Set : A:\Yamamt01.app

Output Set: N:\CRF3\01242001\I435770.raw

L:247 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
M:254 Repeated in SeqNo=7
L:331 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:8
L:535 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:17
M:254 Repeated in SeqNo=17
L:601 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:18
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:922 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:20
L:935 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:21
L:948 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:22
L:961 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:23
L:974 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:24
L:987 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:25
L:1000 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:26
L:1013 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:27
L:1026 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:28
L:1039 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:29
L:1052 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:30
L:1065 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1065 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1065 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
L:1065 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:31
L:1085 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32
differs:33
L:1086 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:32
M:254 Repeated in SeqNo=32
L:1305 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:33
L:1317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:34
L:1330 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:35
L:1343 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:36
L:1356 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:37
L:1369 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:38
L:1382 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:39